

sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences;

(iii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, and (b) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences; or

(iv) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, (b) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (1) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (2) the isolated nucleic acid fragment comprising a full length or partial corn oleosin promoter hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences, and (c) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences; wherein expression of the chimeric gene results in an altered corn stearic acid phenotype.

173. (once amended) A method of improving the carcass quality of an animal by feeding the animal a carcass quality improving amount of animal feed derived from the processing of corn grain obtained from a corn plant or plant part which comprises a chimeric gene selected from the group consisting of:

(i) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, operably linked to suitable regulatory sequences;

(ii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, and (b) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and

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said promoter: (1) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (2) the isolated nucleic acid fragment comprising a full length or partial corn oleosin promoter hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences;

(iii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, and (b) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences; or

(iv) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, (b) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (1) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (2) the isolated nucleic acid fragment comprising a full length or partial corn oleosin promoter hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences, and (c) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences; wherein expression of the chimeric gene results in an altered corn oleic acid phenotype.

174. (once amended) A method of improving the carcass quality of an animal by feeding the animal a carcass quality improving amount of animal feed derived from the processing of corn grain obtained from a corn plant or plant part which comprises a chimeric gene selected from the group consisting of:

(i) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, and a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a

functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, operably linked to suitable regulatory sequences;

(ii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, (b) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, and (c) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (1) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (2) the isolated nucleic acid fragment comprising a full length or partial corn oleosin promoter hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences,

(iii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, (b) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, and (c) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences; or

(iv) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or the reverse complement thereof, (b) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or the reverse complement thereof, (c) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and

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said promoter: (1) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS: 19 or 38-49 or (2) the isolated nucleic acid fragment comprising a full length or partial corn oleosin promoter hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, and (d) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences, wherein expression of the chimeric gene results in an altered corn oil phenotype.

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176. (once amended) A method of improving the carcass quality of an animal by feeding the animal a carcass quality improving amount of animal feed derived from the processing of corn grain obtained from a corn plant or plant part which comprises

(i) a first chimeric gene selected from the group consisting of:

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(a) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS: 9 or 11, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, operably linked to suitable regulatory sequences;

(b) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS: 9 or 11, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, and (2) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (A) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS: 19 or 38-49 or (BB) the isolated nucleic acid fragment comprising a full length or partial corn oleosin promoter hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences;

(c) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS: 9 or 11, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, and (2) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences; or

(d) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second

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polypeptide selected from SEQ ID NOS:9 or 11, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, (2) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (A) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (B) the isolated nucleic acid fragment comprising a full length or partial corn oleosin promoter hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences, and (3) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences, and

(ii) a second chimeric gene selected from the set consisting of:

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(a) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, operably linked to suitable regulatory sequences;

(b) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, and (2) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (A) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (B) the isolated nucleic acid fragment comprising a full length or partial corn oleosin promoter hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences;

(c) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, and (2) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences; or

(d) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set

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forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, (2) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (A) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS: 19 or 38-49 or (B) the isolated nucleic acid fragment comprising a full length or partial corn oleosin promoter hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences, and (3) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences, wherein expression of the chimeric genes results in an altered corn oil phenotype.

Remarks

Claims 172-174 and 176 have been amended to correct a minor typographical error. No change was made to claim 175. Accordingly, no new matter has been added. Claims 172-176 are now pending. A marked-up version of the rewritten claims are attached as a separate page to this amendment and is titled "Version With Markings to Show Changes Made."

Pursuant to the Examiner's request (made in a telephone interview held on Thursday, March 29, 2001), additional copies of the non-patent references previously cited on the Information Disclosure Statement accompany this Supplemental Preliminary Amendment. At this time, copies of all previously cited U.S. Patents are not included.

Please charge any fees which are required in connection with the filing of this Preliminary Amendment to Deposit Account No. 04-1928 (E. I. du Pont de Nemours and Company).

Respectfully submitted,

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Enclosures